



IFW16

RAW SEQUENCE LISTING

DATE: 07/21/2004

PATENT APPLICATION: US/10/023,066B

TIME: 10:46:50

Input Set : A:\BB1037 US DIV1 Corrected Sequence Listing.txt

Output Set: N:\CRF4\07212004\J023066B.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: E. I. DU PONT DE NEMOURS AND
6 COMPANY

8 (ii) TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
9 INCREASING THE LYSINE AND
10 THREONINE CONTENT OF THE SEEDS OF
11 PLANTS

13 (iii) NUMBER OF SEQUENCES: 108

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: E. I. DU PONT DE NEMOURS
17 AND COMPANY

18 (B) STREET: 1007 MARKET STREET

19 (C) CITY: WILMINGTON

20 (D) STATE: DELAWARE

21 (E) COUNTRY: U.S.A.

22 (F) ZIP: 19898

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: FLOPPY DISK

26 (B) COMPUTER: IBM PC COMPATIBLE

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: MICROSOFT WORD VERSION 2.0C

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/10/023,066B

C--> 32 (B) FILING DATE: 17-Dec-2001

33 (C) CLASSIFICATION:

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: BARBARA C. SIEGELL

37 (B) REGISTRATION NUMBER: 30,684

38 (C) REFERENCE/DOCKET NUMBER: BB-1037-C

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 302-992-4931

42 (B) TELEFAX: 302-773-0164

43 (C) TELEX: 835420

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 1350 base pairs

49 (B) TYPE: nucleic acid

50 (C) STRANDEDNESS: single

51 (D) TOPOLOGY: linear

53 (ii) MOLECULE TYPE: DNA (genomic)

55 (ix) FEATURE:

56 (A) NAME/KEY: CDS

(ps. 6)
ENTERED

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57          (B) LOCATION: 1..1350
59      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 ATG GCT GAA ATT GTT GTC TCC AAA TTT GGC GGT ACC AGC GTA GCT GAT      48
62 Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp
63   1           5           10           15
65 TTT GAC GCC ATG AAC CGC AGC GCT GAT ATT GTG CTT TCT GAT GCC AAC      96
66 Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn
67           20           25           30
69 GTG CGT TTA GTT GTC CTC TCG GCT TCT GCT GGT ATC ACT AAT CTG CTG     144
70 Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu
71           35           40           45
73 GTC GCT TTA GCT GAA GGA CTG GAA CCT GGC GAG CGA TTC GAA AAA CTC     192
74 Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu
75           50           55           60
77 GAC GCT ATC CGC AAC ATC CAG TTT GCC ATT CTG GAA CGT CTG CGT TAC     240
78 Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr
79   65           70           75           80
81 CCG AAC GTT ATC CGT GAA GAG ATT GAA CGT CTG CTG GAG AAC ATT ACT     288
82 Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr
83           85           90           95
85 GTT CTG GCA GAA GCG GCG GCG CTG GCA ACG TCT CCG GCG CTG ACA GAT     336
86 Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp
87           100           105           110
89 GAG CTG GTC AGC CAC GGC GAG CTG ATG TCG ACC CTG CTG TTT GTT GAG     384
90 Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu
91           115           120           125
93 ATC CTG CGC GAA CGC GAT GTT CAG GCA CAG TGG TTT GAT GTA CGT AAA     432
94 Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys
95           130           135           140
97 GTG ATG CGT ACC AAC GAC CGA TTT GGT CGT GCA GAG CCA GAT ATA GCC     480
98 Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala
99 145           150           155           160
101 GCG CTG GCG GAA CTG GCC GCG CTG CAG CTG CTC CCA CGT CTC AAT GAA     528
102 Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu
103           165           170           175
105 GGC TTA GTG ATC ACC CAG GGA TTT ATC GGT AGC GAA AAT AAA GGT CGT     576
106 Gly Leu Val Ile Thr Gln Gly Phe Ile Gly Ser Glu Asn Lys Gly Arg
107           180           185           190
109 ACA ACG ACG CTT GGC CGT GGA GGC AGC GAT TAT ACG GCA GCC TTG CTG     624
110 Thr Thr Thr Leu Gly Arg Gly Gly Ser Asp Tyr Thr Ala Ala Leu Leu
111           195           200           205
113 GCG GAG GCT TTA CAC GCA TCT CGT GTT GAT ATC TGG ACC GAC GTC CCG     672
114 Ala Glu Ala Leu His Ala Ser Arg Val Asp Ile Trp Thr Asp Val Pro
115           210           215           220
117 GGC ATC TAC ACC ACC GAT CCA CGC GTA GTT TCC GCA GCA AAA CGC ATT     720
118 Gly Ile Tyr Thr Thr Asp Pro Arg Val Val Ser Ala Ala Lys Arg Ile
119 225           230           235           240
121 GAT GAA ATC GCG TTT GCC GAA GCG GCA GAG ATG GCA ACT TTT GGT GCA     768
122 Asp Glu Ile Ala Phe Ala Glu Ala Ala Glu Met Ala Thr Phe Gly Ala

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123          245          250          255
125 AAA GTA CTG CAT CCG GCA ACG TTG CTA CCC GCA GTA CGC AGC GAT ATC      816
126 Lys Val Leu His Pro Ala Thr Leu Leu Pro Ala Val Arg Ser Asp Ile
127          260          265          270
129 CCG GTC TTT GTC GGC TCC AGC AAA GAC CCA CGC GCA GGT GGT ACG CTG      864
130 Pro Val Phe Val Gly Ser Ser Lys Asp Pro Arg Ala Gly Gly Thr Leu
131          275          280          285
133 GTG TGC AAT AAA ACT GAA AAT CCG CCG CTG TTC CGC GCT CTG GCG CTT      912
134 Val Cys Asn Lys Thr Glu Asn Pro Pro Leu Phe Arg Ala Leu Ala Leu
135          290          295          300
137 CGT CGC AAT CAG ACT CTG CTC ACT TTG CAC AGC CTG AAT ATG CTG CAT      960
138 Arg Arg Asn Gln Thr Leu Leu Thr Leu His Ser Leu Asn Met Leu His
139 305          310          315          320
141 TCT CGC GGT TTC CTC GCG GAA GTT TTC GGC ATC CTC GCG CGG CAT AAT      1008
142 Ser Arg Gly Phe Leu Ala Glu Val Phe Gly Ile Leu Ala Arg His Asn
143          325          330          335
145 ATT TCG GTA GAC TTA ATC ACC ACG TCA GAA GTG AGC GTG GCA TTA ACC      1056
146 Ile Ser Val Asp Leu Ile Thr Thr Ser Glu Val Ser Val Ala Leu Thr
147          340          345          350
149 CTT GAT ACC ACC GGT TCA ACC TCC ACT GGC GAT ACG TTG CTG ACG CAA      1104
150 Leu Asp Thr Thr Gly Ser Thr Ser Thr Gly Asp Thr Leu Leu Thr Gln
151          355          360          365
153 TCT CTG CTG ATG GAG CTT TCC GCA CTG TGT CGG GTG GAG GTG GAA GAA      1152
154 Ser Leu Leu Met Glu Leu Ser Ala Leu Cys Arg Val Glu Val Glu Glu
155          370          375          380
157 GGT CTG GCG CTG GTC GCG TTG ATT GGC AAT GAC CTG TCA AAA GCC TGC      1200
158 Gly Leu Ala Leu Val Ala Leu Ile Gly Asn Asp Leu Ser Lys Ala Cys
159 385          390          395          400
161 GCC GTT GGC AAA GAG GTA TTC GGC GTA CTG GAA CCG TTC AAC ATT CGC      1248
162 Ala Val Gly Lys Glu Val Phe Gly Val Leu Glu Pro Phe Asn Ile Arg
163          405          410          415
165 ATG ATT TGT TAT GGC GCA TCC AGC CAT AAC CTG TGC TTC CTG GTG CCC      1296
166 Met Ile Cys Tyr Gly Ala Ser Ser His Asn Leu Cys Phe Leu Val Pro
167          420          425          430
169 GGC GAA GAT GCC GAG CAG GTG GTG CAA AAA CTG CAT AGT AAT TTG TTT      1344
170 Gly Glu Asp Ala Glu Gln Val Val Gln Lys Leu His Ser Asn Leu Phe
171          435          440          445
173 GAG TAA      1350
174 Glu *

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W-->

175 450

177 (2) INFORMATION FOR SEQ ID NO: 2:

179 (i) SEQUENCE CHARACTERISTICS:

180 (A) LENGTH: 36 base pairs

181 (B) TYPE: nucleic acid

182 (C) STRANDEDNESS: single

183 (D) TOPOLOGY: linear

185 (ii) MOLECULE TYPE: DNA (genomic)

187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

189 GATCCATGGC TGAAATTGTT GTCTCCAAAT TTGGCG

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RAW SEQUENCE LISTING

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191 (2) INFORMATION FOR SEQ ID NO: 3:
193     (i) SEQUENCE CHARACTERISTICS:
194         (A) LENGTH: 36 base pairs
195         (B) TYPE: nucleic acid
196         (C) STRANDEDNESS: single
197         (D) TOPOLOGY: linear
199     (ii) MOLECULE TYPE: DNA (genomic)
201     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
203 GTACCGCCAA ATTTGGAGAC AACAATTTCA GCCATG          36
205 (2) INFORMATION FOR SEQ ID NO: 4:
207     (i) SEQUENCE CHARACTERISTICS:
208         (A) LENGTH: 48 base pairs
209         (B) TYPE: nucleic acid
210         (C) STRANDEDNESS: single
211         (D) TOPOLOGY: linear
213     (ii) MOLECULE TYPE: DNA (genomic)
215     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
217 CCCGGGCCAT GGCTACAGGT TTAACAGCTA AGACCGGAGT AGAGCACT  48
219 (2) INFORMATION FOR SEQ ID NO: 5:
221     (i) SEQUENCE CHARACTERISTICS:
222         (A) LENGTH: 37 base pairs
223         (B) TYPE: nucleic acid
224         (C) STRANDEDNESS: single
225         (D) TOPOLOGY: linear
227     (ii) MOLECULE TYPE: DNA (genomic)
229     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
231 GATATCGAAT TCTCATTATA GAACTCCAGC TTTTTC          37
233 (2) INFORMATION FOR SEQ ID NO: 6:
235     (i) SEQUENCE CHARACTERISTICS:
236         (A) LENGTH: 917 base pairs
237         (B) TYPE: nucleic acid
238         (C) STRANDEDNESS: single
239         (D) TOPOLOGY: linear
241     (ii) MOLECULE TYPE: DNA (genomic)
243     (ix) FEATURE:
244         (A) NAME/KEY: CDS
245         (B) LOCATION: 3..911
247     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
249 CC ATG GCT ACA GGT TTA ACA GCT AAG ACC GGA GTA GAG CAC TTC GGC      47
250 Met Ala Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly
251   1           5           10          15
253 ACC GTT GGA GTA GCA ATG GTT ACT CCA TTC ACG GAA TCC GGA GAC ATC      95
254 Thr Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile
255           20           25           30
257 GAT ATC GCT GCT GGC CGC GAA GTC GCG GCT TAT TTG GTT GAT AAG GGC     143
258 Asp Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly
259           35           40           45
261 TTG GAT TCT TTG GTT CTC GCG GGC ACC ACT GGT GAA TCC CCA ACG ACA     191
262 Leu Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr

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263          50          55          60
265 ACC GCC GCT GAA AAA CTA GAA CTG CTC AAG GCC GTT CGT GAG GAA GTT 239
266 Thr Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val
267          65          70          75
269 GGG GAT CGG GCG AAG CTC ATC GCC GGT GTC GGA ACC AAC AAC ACG CGG 287
270 Gly Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg
271 80          85          90          95
273 ACA TCT GTG GAA CTT GCG GAA GCT GCT GCT TCT GCT GGC GCA GAC GGC 335
274 Thr Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly
275          100          105          110
277 CTT TTA GTT GTA ACT CCT TAT TAC TCC AAG CCG AGC CAA GAG GGA TTG 383
278 Leu Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu
279          115          120          125
281 CTG GCG CAC TTC GGT GCA ATT GCT GCA GCA ACA GAG GTT CCA ATT TGT 431
282 Leu Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys
283          130          135          140
285 CTC TAT GAC ATT CCT GGT CGG TCA GGT ATT CCA ATT GAG TCT GAT ACC 479
286 Leu Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr
287          145          150          155
289 ATG AGA CGC CTG AGT GAA TTA CCT ACG ATT TTG GCG GTC AAG GAC GCC 527
290 Met Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala
291 160          165          170          175
293 AAG GGT GAC CTC GTT GCA GCC ACG TCA TTG ATC AAA GAA ACG GGA CTT 575
294 Lys Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu
295          180          185          190
297 GCC TGG TAT TCA GGC GAT GAC CCA CTA AAC CTT GTT TGG CTT GCT TTG 623
298 Ala Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu
299          195          200          205
301 GGC GGA TCA GGT TTC ATT TCC GTA ATT GGA CAT GCA GCC CCC ACA GCA 671
302 Gly Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala
303          210          215          220
305 TTA CGT GAG TTG TAC ACA AGC TTC GAG GAA GGC GAC CTC GTC CGT GCG 719
306 Leu Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala
307          225          230          235
309 CGG GAA ATC AAC GCC AAA CTA TCA CCG CTG GTA GCT GCC CAA GGT CGC 767
310 Arg Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg
311 240          245          250          255
313 TTG GGT GGA GTC AGC TTG GCA AAA GCT GCT CTG CGT CTG CAG GGC ATC 815
314 Leu Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile
315          260          265          270
317 AAC GTA GGA GAT CCT CGA CTT CCA ATT ATG GCT CCA AAT GAG CAG GAA 863
318 Asn Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu
319          275          280          285
321 CTT GAG GCT CTC CGA GAA GAC ATG AAA AAA GCT GGA GTT CTA TAA TGAGAATTC 917
322 Leu Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu *
323          290          295          300
325 (2) INFORMATION FOR SEQ ID NO: 7:
327 (i) SEQUENCE CHARACTERISTICS:
328 (A) LENGTH: 22 base pairs

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/21/2004
PATENT APPLICATION: US/10/023,066B TIME: 10:46:51

Input Set : A:\BB1037 US DIV1 Corrected Sequence Listing.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:93; N Pos. 557,558,559,560,561

Seq#:102; N Pos. 97

Seq#:103; N Pos. 253,289,293

Seq#:104; Xaa Pos.32

VERIFICATION SUMMARY

DATE: 07/21/2004

PATENT APPLICATION: US/10/023,066B

TIME: 10:46:51

Input Set : A:\BB1037 US DIV1 Corrected Sequence Listing.txt

Output Set: N:\CRF4\07212004\J023066B.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
 L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
 L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:775 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:842 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
 L:1379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
 L:2635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:16